Sara Guirao-Rico

List of Publications by Year
in descending order

20 papers	**4,875** citations	840585 **11** h-index	752573 **20** g-index
23 all docs	**23** docs citations	**23** times ranked	**7587** citing authors

#	Article	IF	Citations
1	Population-scale long-read sequencing uncovers transposable elements associated with gene expression variation and adaptive signatures in Drosophila. Nature Communications, 2022, 13, 1948.	5.8	53
2	Temperature, rainfall and wind variables underlie environmental adaptation in natural populations of <i>Drosophila melanogaster</i>. Molecular Ecology, 2021, 30, 938-954.	2.0	15
3	Benchmarking the performance of Pool€seq SNP callers using simulated and real sequencing data. Molecular Ecology Resources, 2021, 21, 1216-1229.	2.2	19
4	<i>Drosophila</i> Evolution over Space and Time (DEST): A New Population Genomics Resource. Molecular Biology and Evolution, 2021, 38, 5782-5805.	3.5	37
5	Evolutionary History of Major Chemosensory Gene Families across Panarthropoda. Molecular Biology and Evolution, 2020, 37, 3601-3615.	3.5	10
6	Evolutionary insights from large scale resequencing datasets in Drosophila melanogaster. Current Opinion in Insect Science, 2019, 31, 70-76.	2.2	8
7	Population€specific dynamics and selection patterns of transposable element insertions in European natural populations. Molecular Ecology, 2019, 28, 1506-1522.	2.0	45
8	Porcine Y-chromosome variation is consistent with the occurrence of paternal gene flow from non-Asian to Asian populations. Heredity, 2018, 120, 63-76.	1.2	14
9	Sequence diversity patterns suggesting balancing selection in partially sex€linked genes of the plant <i>Silene latifolia</i> are not generated by demographic history or gene flow. Molecular Ecology, 2017, 26, 1357-1370.	2.0	17
10	DnaSP 6: DNA Sequence Polymorphism Analysis of Large Data Sets. Molecular Biology and Evolution, 2017, 34, 3299-3302.	3.5	4,056
11	Computational prediction of the phenotypic effects of genetic variants: basic concepts and some application examples in Drosophila nervous system genes. Journal of Neurogenetics, 2017, 31, 307-319.	0.6	2
12	Recombination changes at the boundaries of fully and partially sex-linked regions between closely related Silene species pairs. Heredity, 2017, 118, 395-403.	1.2	19
13	DOMINO: development of informative molecular markers for phylogenetic and genome-wide population genetic studies in non-model organisms. Bioinformatics, 2016, 32, 3753-3759.	1.8	8
14	<scp>RAD</scp> mapping reveals an evolving, polymorphic and fuzzy boundary of a plant pseudoautosomal region. Molecular Ecology, 2016, 25, 414-430.	2.0	29
15	Comparative analysis of tissue-specific transcriptomes in the funnel-web spider<i>Macrothele calpeiana</i>(Araneae, Hexathelidae). PeerJ, 2015, 3, e1064.	0.9	14
16	Patterns of Nucleotide Diversity at the Regions Encompassing the Drosophila Insulin-Like Peptide (dilp) Genes: Demography vs. Positive Selection in Drosophila melanogaster. PLoS ONE, 2013, 8, e53593.	1.1	1
17	Molecular Population Genetics of the Insulin/TOR Signal Transduction Pathway: A Network-Level Analysis in Drosophila melanogaster. Molecular Biology and Evolution, 2012, 29, 123-132.	3.5	17
18	Molecular Evolution of the Ligands of the Insulin-Signaling Pathway: dilp Genes in the Genus Drosophila. Molecular Biology and Evolution, 2011, 28, 1557-1560.	3.5	6

#	Article	IF	Citations
19	Genome sequences of the human body louse and its primary endosymbiont provide insights into the permanent parasitic lifestyle. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 12168-12173.	3.3	482
20	Positive Selection Has Driven the Evolution of the Drosophila Insulin-Like Receptor (InR) at Different Timescales. Molecular Biology and Evolution, 2009, 26, 1723-1732.	3.5	11